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ACGTTGACAC AGGAATGAAG AGTGTATTGG CTGAATCTTC AAGCAGAGGC GATATTGACC ATGTGCTTT TAAATTGGCC TCGCTGACCC GCCCCTTGG TGTAAAAGAA GAACCGGCCA AAGGGAGGGC CTGAAGGACC TCCACAGGAG TGTGAGCAGC ACTGCTTCAG CAACAAAGCC TCAGGTCCAC ATCTTGGAA GAAT ATG GCC ACT TCC TGG GGG GCT GTC TTC Met Ala Thr Ser Trp Gly Ala Val Phe 1 5	60 120 180 231
ATG CTG ATC ATA GCC TGC GTT GGC AGC ACT GTC TTC TAC AGA GAA CAG Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln 10 15 20 25	279
CAG ACC TGG TTT GAA GGT GTC TTC TTG TCT TCC ATG TGC CCC ATT AAT Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn 30 35 40	327
GTC AGT GCC GGC ACC TTT TAT GGA ATT ATG TTT GAT GCG GGC AGC ACT Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr 45 50 55	375
GGA ACT CGG ATT CAT GTT TAC ACT TTT GTG CAG AAA ACA GCA GGA CAG Gly Thr Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln 60 65 70	423
CTC CCC TTT CTG GAA GGT GAA ATT TTT GAT TCT GTG AAG CCG GGA CTT Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu 75 80 85	471
TCT GCT TTT GTG GAT CAG CCC AAA CAG GGT GCT GAG ACT GTC CAG GAG Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu 90 95 100 105	519
CTC TTG GAG GTG GCC AAA GAC TCG ATC CCC AGA AGC CAC TGG GAA AGG Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg 110 115 120	567
ACC CCG GTG GTT CTG AAA GCA ACG GCC GGA CTC CGT TTG CTG CCT GAG Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Pro Glu 125 130 135	615
CAG AAA GCC CAG GCT CTG CTC TTG GAG GTA GAG GAG ATC TTC AAG AAT Gln Lys Ala Gln Ala Leu Leu Glu Val Glu Ile Phe Lys Asn 140 145 150	663
TCA CCT TTC CTG GTC CCA GAT GGC AGC GTC AGC ATC ATG GAT GGG TCC Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser 155 160 165	711
TAT GAA GGC ATA CTA GCC TGG GTT ACC GTG AAC TTT CTA ACA GGT CAG Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln 170 175 180 185	759
CTG CAT GGT CGT GGC CAG GAG ACT GTG GGG ACC CTT GAC CTG GGG GGT Leu His Gly Arg Gly Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gln 190 195 200	807
GCC TCC ACC CAA ATC ACG TTT CTA CCC CAG TTT GAG AAA ACC CTG GAA Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu 205 210 215	855
CAA ACA CCT AGG GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr 220 225 230	903

Fig. 1

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TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala 235 240 245	951
AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His 250 255 260 265	999
ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile 270 275 280	1047
TTT GGG GGT GTG AAA TAC CAG TAT GGT GGT AAC CAA GAA GGG GAG ATG Phe Gly Gly Val Lys Tyr Gln Tyr Gly Asn Gln Glu Gly Glu Met 285 290 295	1095
GGC TTT GAA CCC TGC TAT GCG GAA GTG CTG AGG GTA GTA CAG GGG AAA Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys 300 305 310	1143
CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC GCC TTC TAC GCT TTC TCT Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser 315 320 325	1191
TAC TAC TAC GAT CGA GCC GCT GAC ACA CAC TTG ATC GAT TAT GAA AAG Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys 330 335 340 345	1239
GGC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val 350 355 360	1287
TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met 365 370 375	1335
GAC CTC ACT TAC ATC ACA GCC CTG TTG AAA GAT GGT TTG GGC TTT GCC Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala 380 385 390	1383
GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp 395 400 405	1431
TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT Trp Leu Gly Leu Gly His Leu Ser Pro Ala Pro Val Ser Gly His 410 415 420 425	1479
CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro 430 435 440	1527
GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser 445 450 455	1575
GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGGTTTT Gly Lys Ala Trp Pro Glu Thr Arg 460 465	1629

Fig. 1 (cont'd.)

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TAGATGAGTC	TTGCTCTTGA	GCCTAGTGAT	TTGGGCTTCA	ATGATTTGCA	CATCTAAATGT	1689
GAATAGTCCTC	TAACCACTTG	GTGGGTGCAT	GCCTGGCACC	AGACTGTAAA	TCTTTTGGGA	1749
TTCTTTGTAC	AGAGCTCTGC	AAAGAAAAAA	AGAGAAAAAGG	TTTGGGAATC	CATGCTAGAT	1809
TCGGAGATTC	GAACGACAGGTC	CTCTGGGACC	AAAAGAACAT	CTCTGGTCAAA	CCCTGGGATG	1869
CCTCATTGCT	TTGAATGGAT	TCATTTTGC	TTATAAGCTG	ATTTACTGAA	ATCCCCATAAC	1929
CCATCAATGC	TGTAAATTTT	TTTCTTCCTA	CCCTTATTAC	ATTCCTTACCC	CTAAAAGCCT	1989
GGGGGAAATA	CCTGGTTTTC	CTTCCCACATCT	ATAATTGAGA	AAGAGGGGGG	AAAAGATACT	2049
GTATTTAGAAT	TTGTGTGATC	CTGTGGCACA	ATAGATCAAC	CAACCCATT	AAAGCTTAAA	2109
AAAAAAAAAA						2119

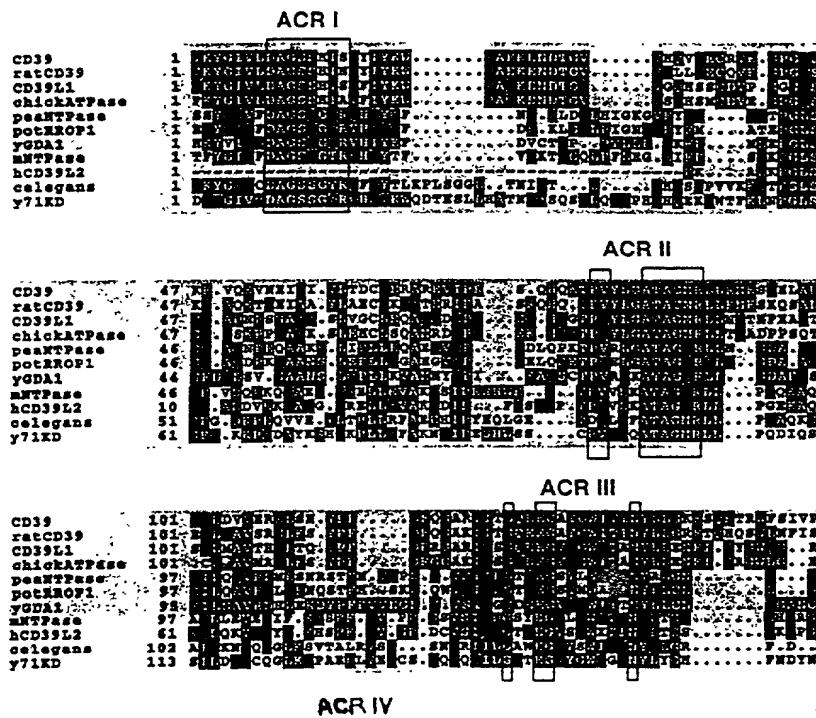
FIG. 1 (cont'd.)

peaNTPase	1	----HELLRNLITYFLPSMBAITSSOYQGNELTSRHFCKQDESISSYAVVFDAGSTGSR
potapyrase	1	SLNQNSHSPFIIHMMFLVPLSLSKRNNAQDPRRHILSNESEHYAVVFDAGSTGSR
mNTPase	1	SATSGAGPMLIACVQSTVYIREQQTWEGEPSSMCPNVSAGAFYCEVNFADAGSTGSR
yGDPase	1	KTPWMIHSLPXPNDPEGLQDQKTEONYPPELADAYKQSQTSEEHAYVINTDAGSTGSR
peaNTPase	57	LVHVYEFNQMLDHLHICKGVEMYKATPGLSSXAMPQOAAASLIPILEAEEDVVFDDLQP
potapyrase	59	VHVVFDFDRLGLLPIGNNIYFMADEPGLSSYALDPKAAAMSLLPLLGCAESVVFQNLQS
mNTPase	61	LVHVTFVORTAGOLPFBEGEMFDEMKPGLSAATVHOPKOGGETVQELLEVARSDIPRSHWE
yGDPase	61	YHIMKFDVCTQ.EPPTLDEKFDMLPEGLSSEDTDSVGRANSLPPLKVAWVYPIKARS
peaNTPase	117	KTPVRLGATAGLRLLNCDASEKILOSVRDNLMLRSTF.NVQPDWVSIAGTQEGSYLVWT
potapyrase	119	ETPDEULGATAGLRLMNCDASEKILQAVENHVKNSDF.HSDQVWVTFDGTQEGSYLWAN
mNTPase	121	ATPVVVKATAGLRLLPDKACALMLLEWENLCKM.SPF.WPFDGIVSIMDGVEGILIAWVT
yGDPase	119	CTPVAVKATAGLRLLCAKSKILSAVRDNLMLDTPYEGDQVSINGCDEEGVIAWIT
peaNTPase	176	VNVVALGNLNGKAKTK.TVGVIDLGGGSVQNAVAVSKKQHNAKPKWADGDPYVKKVVLKG
potapyrase	178	INVLLGNGLKGDKMS.TTATIDBLGCGGSVQNAVAVSKQHNAKPKWADGDPYVKKVVLKG
mNTPase	179	VNLLTGTGQHKGEGQE.TVGVIDLGGGATQKELPQPEK...TLEQTPROGLTSPENFN
yGDPase	179	TNYLLGNGCANGPKLFLAAWFDLGGGATQKELPQPEK...TLEQTPROGLTSPENFN
peaNTPase	224	IPWCLVYVHSYVHFGRAASRAELNL.....
potapyrase	225	KDPLVYVHSYVHFGRAASRAELNL.....
mNTPase	226	STEKLWTHSINGFGKKAALATDGA.....
yGDPase	234	ENHTLYOFSHLGYGLKECHNKNVSVENALKDGIKLGDNTPHCLSSPCIPPKVNAKTN
peaNTPase	276	TYSGPBPKAVATYTSGW.....NPKNCNTTIRKALKLNYPCPYCNCTFGGMNNGGGGN.....
potapyrase	277	SGCGYVYKVNAPKXG.....SFKRCCRRLTHALKINACMHECTENGVWNGGGGD.....
mNTPase	270	KCCPRWLRDRENWIFCGV.....KXQYGGNQEGEMGFPFCYAKELRIVYVQGKLNHQPEEVN.....
yGDPase	294	EKVTLSKETYTIDFIGDPEPQAOCPPLDDEIENKDAQCGSPPCBENGVHQPSLVLNPK
peaNTPase	328	GOKNCASSSEMYLPEDTGHVIDXSTENFMDPFDIETKAKEACALNEPDKSAEPLDKE
potapyrase	329	GOKNCASSSEYDGAQGIVDTKFPSAALKPLQYLNAAKVACOMVADTSEKISSEKTQK
mNTPase	322	CSA.FYAFSYDYYDRAADTHEIYQE.KGGVYKLVDFERKAREYCH.SLGSPFSGCP.....
yGDPase	354	ESNDKMYIFSYDHTTRPLGMLPQHNPMLNDLARIVCKGEESWNSVVECHAGS...HDEL
peaNTPase	388	WQASVYCMDDLYIQYVLLVDGFGLDQKQKTRGRKLEIYQHATIPLAAMBLGCVVAVASJLPR
potapyrase	389	NN.PYLCMDLILYRMLLVDGFGLDQKQKTRGRKLEIYQHATIPLAAMBLGCVVAVASJLPR
mNTPase	374	...EICMDLITYTALLMDGCPAERHPYQHRESEOPRDWLGLGQHLSFAPVSGHQLR
yGDPase	411	ESDSHFCFLDLSPOVSLHMTGKDIPLQREHRTGKMANK...IOWCLGASEPELKADNW
peaNTPase	448	PERGNYFV-----
potapyrase	448	MIRYASH-----
mNTPase	430	PSSTAEACISZEPVFSQEGVDSETPSDLSGKANPETR-----
yGDPase	467	CKKNSA-----

FIG. 2

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F16.3

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GTGGGGTCGT ATCCCGCGGG TGGAGGCCGG GGTGGCGCCG GCCGGGGCGG GGGAGCCAA	60
AAGACCGGCT GCCGCCTGCT CCCCCGAAAA GGGCACTCGT CTCCGTGGGT GTGGCGGAGC	120
CGCGGGTGCAG TGGATGGGC TATGTGAATG AAAAAGGTA TCCGTTATGA AACTCCAGA	180
AAAACGAGCT ACATTTTCA GCAGCCGCAG CACGGTCCTT GGCAAACAAG G ATG AGA	237
Met Arg	
1	
AAA ATA TCC AAC CAC GGG AGC CTG CGG GTG GCG AAG GTG GCA TAC CCC	285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro	
5 10 15	
CTG GGG CTG TGT GTG GGC GTG TTC ATC TAT GTT GCC TAC ATC AAG TGG	333
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp	
20 25 30	
CAC CGG GCC ACC GCC ACC CAG GCC TTC TTC AGC ATC ACC AGG GCA GCC	381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala	
35 40 45 50	
CCG GGG GCC CGG TGG GGT CAG CAG GCC CAC AGC CCC CTG GGG ACA GCT	429
Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala	
55 60 65	
GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC	477
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser	
70 75 80	
ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CCG CCC CCC AGA GAA	525
Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu	
85 90 95	
ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT	573
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu	
100 105 110	
TCT GCC TAT GCT GAT GAT GTT GAA AAG AGC GCT CAG GGA ATC CGG GAA	621
Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu	
115 120 125 130	
CTA CTG GAT GTT GCT AAA CAG GAC ATT CCG TTC GAC TTC TGG AAG GCC	669
Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala	
135 140 145	
ACC CCT CTG GTC CTC AAG GCC ACA GCT GGC TTA CGC CTG TTA CCT GGA	717
Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly	
150 155 160	
GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA	765
Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala	
165 170 175	
TCG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA	813
Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr	
180 185 190	
GAT GAA GGC GTT TCG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC	861
Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser	
195 200 205 210	
TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA	909
Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly	
215 220 225	

FIG. 4

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GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln 230 235 240	957
GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr 245 250 255	1005
TAC AAG CTC TAT TCC TAC AGC TAC CTC GGG CTC GGG CTG ATG TCG GCA Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala 260 265 270	1053
CGC CTG GCG ATC CTG GGC GGC GTG GAG GGG CAG CCT GCT AAG GAT GGA Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly 275 280 285 290	1101
AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp 295 300 305	1149
GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala 310 315 320	1197
AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn 325 330 335	1245
AGA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe 340 345 350	1293
TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu 355 360 365 370	1341
AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr 375 380 385	1389
GTG TGT CGG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys 390 395 400	1437
ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG GAG TTC GGC TTT CCC Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro 405 410 415	1485
AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr 420 425 430	1533
AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg 435 440 445 450	1581
CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTAG CAGTGTCT Gln Lys Ser Pro Ala Ser 455	1637
GTGTGTCTGC ATAAACCCCTC CTGTCTGGGA CGTGACTTCA TCCTGAGGAG CCACAGCACA GGCCGTGCTG GCACTTTCTG CACACTGGCT CTGGGACTTG CAGAAGGGCTT GGTGCTGCC TGGCATCAGC CTCTTCCAGT CACATCTGGC CAGAGGGCTG TCTGGACCTG GGCCCTGCTC 1697 1757 1817	

FIG. 4 (cont'd.)

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AATGCCACCT	GTCTGCCTGG	GCTCCAAGTG	GGCAGGGACCA	GGACAGAACCC	ACAGGCACAC	1877
ACTGAGGGGG	CAGTGTGGCT	CCCTGCCTGT	CCCATCCCCA	TGCCCCGTCC	GCGGGGCTGT	1937
GGCTGCTGCT	GTGCATGTCC	CTGGCATGGG	AGTCTTGTCT	CCCAGCCTGT	CAGTTTCTC	1997
CCCAGGGCAG	AGCTCCCTT	CCTGCAAGAG	TCTGGGAGGC	GGTGCAGGCT	GTCTGGCTG	2057
CTCTGGGAA	GCCGAGGGAC	AGCCATAACA	CCCCCGGGAC	AGTAGGTCTG	GGCGGCACCA	2117
CTGGGAACTC	TGGACTTGAG	TGTGTTGCT	CTTCCTTGGG	TATGAATGTG	TGAGTTCA	2177
CAGAGGCCTG	CTCTCCTCAC	ACATTGTGTG	GTTGGGGTT	AATGATGGAG	GGAGACACCT	2237
CTTCATAGAC	GGCAAGTGCC	CACCTTCAG	GGAGTCTCCC	AGCATGGGCG	GATGCCGGC	2297
ATGAGCTGCT	GTAAACTATT	TGTGGCTGTG	CTGCTTGAGT	GACGTCTCTG	TCGTGTGGGT	2357
GCCAAGTGCT	TGTGTAGAAA	CTGTGTTCTG	AGCCCCCTTT	TCTGGACACC	AACTGTGTCC	2417
TGTGAATGTA	TCGCTACTGT	GAGCTGTTCC	CGCCTAGCCA	GGGCCATGTC	TTAGGTGCAG	2477
CTGTGCCACG	GGTCAGCTGA	GCCACAGTCC	CAGAACCAAG	CTCTCGGTGT	CTCGGGCCAC	2537
CATCCGCCCA	CCTCGGGCTG	ACCCCCACCTC	CTCCATGGAC	AGTGTGAGCC	CCGGGCCGTG	2597
CATCCTGCTC	AGTGTGGCGT	CAGTGTGGG	GCTGAGCCCC	TTGAGCTGCT	TCAGTGAATG	2657
TACAGTGCC	GGCACGAGCT	GAACCTCATG	TGTTCCACTC	CCAATAAAAG	GTTGACAGGG	2717
GCTTCTCCTT	CAAAAAAAA	AAAAAAA	AAAAAAA	AAAAA		2762

Fig. 4 (cont'd)

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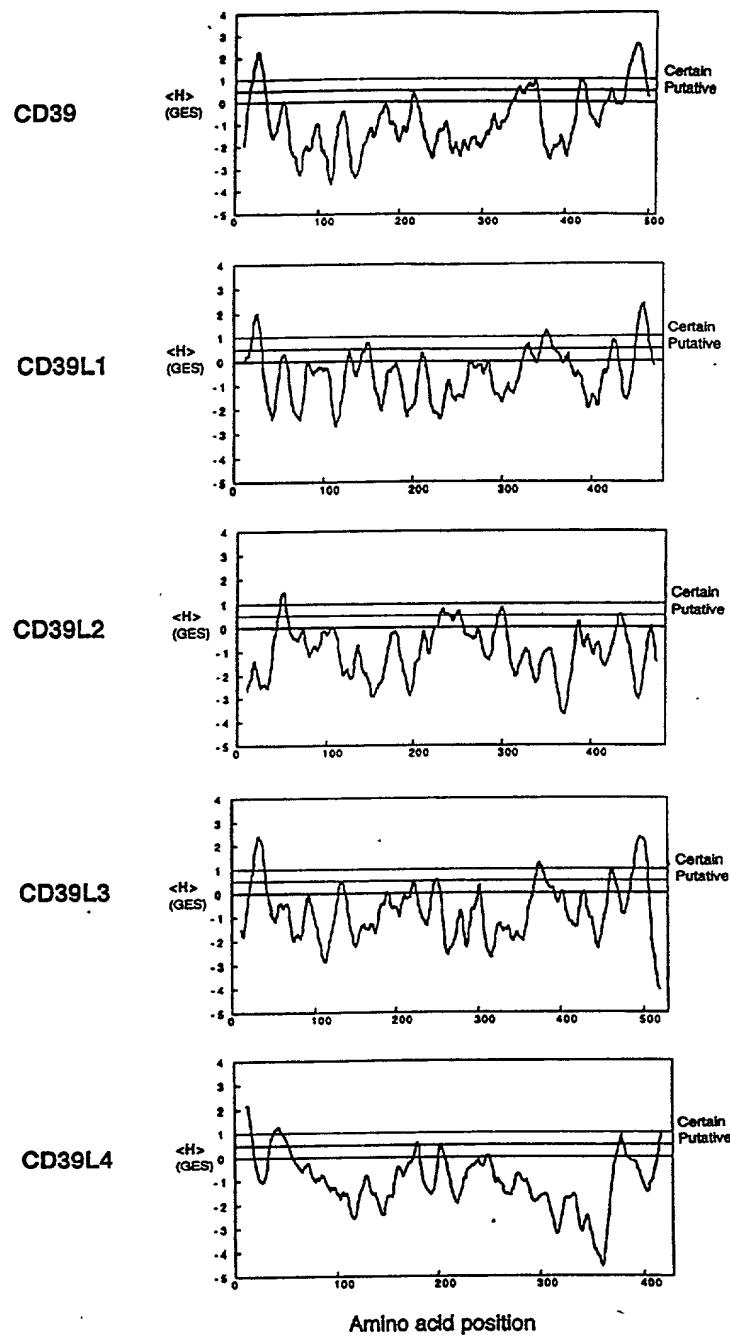


FIG. 5

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ACCCACCGCGT CTGGCCGCAG CGCCGCCTCTG CGGCAGCGCT AGTCGCCTTC TCCGAATCGG CTCCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT Met Phe Thr Val Leu Thr Arg Gln Pro Cys 1 5 10	60 112
GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala 15 20 25	160
TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val 30 35 40	208
ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly 45 50 55	256
ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln 60 65 70	304
TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe 75 80 85 90	352
AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro 95 100 105	400
CAA GAT GTC CCC AGA GCC TTT GAG GAG TGT ATG CAA AAA GTC AAG GGG Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly 110 115 120	448
CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala 125 130 135	496
ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn 140 145 150	544
GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp 155 160 165 170	592
TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GAA GGG GTA TAT GGA Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly 175 180 185	640
TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu 190 195 200	688
TGG CAC ATG TGG GTG CAC CCG CAT GGA GTG GAA ACC ACG GGT GCC CTG Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu 205 210 215	736
GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC TTC GTG GCA GGA GAG AAG Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys 220 225 230	784

Fig. 6

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ATG GAT CTG AAC ACC AGC GAC ATC ATG CAG GTG TCC CTG TAT GGC TAC Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr 235 240 245 250	832
GTA TAC ACG CTC TAC ACA CAC AGC TTC CAG TGC TAT GGC CGG AAT GAG Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu 255 260 265	880
GCT GAG AAG AAG TTT CTG GCA ATG CTC CTG CAG AAT TCT CCT ACC AAA Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys 270 275 280	928
AAC CAT CTC ACC AAT CCC TGT TAC CCT CGG GAT TAT AGC ATC AGC TTC Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe 285 290 295	976
ACC ATG GGC CAT GTA TTT GAT AGC CTG TGC ACT GTG GAC CAG AGG CCA Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro 300 305 310	1024
GAA AGT TAT AAC CCC AAT GAT GTC ATC ACT TTT GAA GGA ACT GGG GAC Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp 315 320 325 330	1072
CCA TCT CTG TGT AAG GAG AAG GTG GCT TCC ATA TTT GAC TTC AAA GCT Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala 335 340 345	1120
TGC CAT GAT CAA GAA ACC TGT TCT TTT GAT GGG GTT TAT CAG CCA AAG Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys 350 355 360	1168
ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC ACA GCC AGT Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser 365 370 375	1216
GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser 380 385 390	1264
ACC TGG AAT TTC TGC TCA CAG AAT TGG AGT CAG CTC CCA CTG CTG CTC Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu 395 400 405 410	1312
CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn 415 420 425	1360
TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr 430 435 440	1408
TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala 445 450 455	1456
TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu 460 465 470	1504
AGC CCT CTG ATC CGT CTG CCC ATA GAA CCA CCT GTC TTT GTG GGC ACC Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr 475 480 485 490	1552

FIG. 6 (cont'd.)

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CTC GCT TTC TTC ACA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala 495 500 505	1600
TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe 510 515 520	1648
GAC CAT GCA GTG GAT TCT GAC TGAGCCTTCA AAGCAGCTCC TGGAGTCCAA TGGC Asp His Ala Val Asp Ser Asp 525	1703
TGCTTAGAGT CAGCCTGGT GGCACCAAGGC AATGCAGGTG AAGTGGCTGC CTTCAAGAAA TACAACTAAC TAAAATCAAAC CACCTAGGTC ACGTGCTCT CAAATACTGA TTTCTGCCAC AGCACCTCTT GAGGCATCCC TTGGCTATTTC TGTCATATT GTTCTTCAGA GACCTCACTA CCCACATGCT GATCTATTGG GGAACAGAGA AGAGACAGGC CACTAAGGTG AGGCTCTTA TATTAAGTTC CCCAGAGGAA GAGTAAGTTG AGAAGGTATC AGTTTAAATGT TGAAAGATTG ACCTCAGGGC TCAGTTTCCA TTTCCCTCCC TCAGTATTCT TCCTGGCAAG ATACCCATTA AGCATTTCGC CAATCAGAAT CTCACTTTAT AGTTTTTCCC ATTGGTCTTT AACTAAAGACT TTCTGTAGC AATCTCGAA GCAGTGAACC CCCTCAGATC AGTAAATAT AGTATCTGGG GGAGAAGACT TACTTCCCTTC AGGGCAGCAG CCACAGCCAG GCTTCTGTCA TACAGGTAGA TCCCGAAGCA CAGAGACATA AAAAAGGTCT CCCAGAAAAC TATAGACCAT TCTCCAAGTG GAATTCCAC TTAGGGCTCT GGTCACTAGA TTGCAACCTG TGTGTTTGTC ATCATCCTCA TCTCACCATT GTATTGCTAT GCCCCTCCCAT AAAAACACAT TGATCCTCTAG CAAGATTATT GCATTCAGA TTTTACTGCC TTTGCTAGGC TTTGCTTAGC CAAAGGGCTG ACTTTCCATT GTTATCATGG TGTATATATT TTTGTCACCA TTCCCACAAAG TATACTTGAT GTTGTCTAG AACGAACATC CTACTCTATG ATTTACTAAC CAATTACTTT CCCAGATCAT AGACCTCTCT GCATAGTAGT CATAAGGTCTT GACTTTGGG AAAGAAAAGG AAGCTGCAGG AATATTATC TCCAAAGTCG AATGAGAAAG AACTCCAGCA AATCCAATGG CTACAAACTA AAAATCAGCA TTATTCATA TTGCTGTTTC TTAGCTGAAT ATGGAATAAA GAACTATTAT TTTATTTGA AAAAAAAAA AAAA	1763 1823 1883 1943 2003 2063 2123 2183 2243 2303 2363 2423 2483 2543 2603 2663 2723 2783 2797

Fig. 6 (cont'd.)

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GGCGCGCGGT TTTCTTGTT CCTGGTCAAC AAAGAAATGT GGAGTGTCTT GGCTGAATCC TCATACAGAC AAGATCATTA TGGTGCTGTT AGGTAGGACT TGTATCCAGA TGTAAGGTTG AAAAGTGTATATAAAGG AACCAAGGAG AAAATTCAAGA AGGAAAGAAA AAATTGCCTC TGCAGGTGTG CGACCGAGAT TGCTTCTGCA ACAAAAGCCT CCACCCAGCC ACATCTTGGG AAAAGA ATG GCC ACT TCT TGG GGC ACA GTC TTT TTC ATG CTG GTG GTA Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val	60 120 180 240 288
1 5 10	
TCC TGT GTT TGC AGC GCT GTC TCC CAC AGG AAC CAG CAG ACT TGG TTT Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe 15 20 25 30	336
GAG GGT ATC TTC CTG TCT TCC ATG TGC CCC ATC AAT GTC AGC GCC AGC Glu Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser 35 40 45	384
ACC TTG TAT GGA ATT ATG TTT GAT GCA GGG AGC ACT GGA ACT CGA ATT Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile 50 55 60	432
CAT GTT TAC ACC TTT GTG CAG AAA ATG CCA GGA CAG CTT CCA ATT CTA His Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu 65 70 75	480
GAA GGG GAA GTT TTT GAT TCT GTG AAG CCA GGA CTT TCT GCT TTT GTA Glu Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val 80 85 90	528
GAT CAA CCT AAG CAG GGT GCT GAG ACC GTT CAA GGG CTC TTA GAG GTG Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val 95 100 105 110	576
GCC AAA GAC TCA ATC CCC CGA AGT CAC TGG AAA AAG ACC CCA GTG GTC Ala Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val 115 120 125	624
CTA AAG GCA ACA GCA GGA CTA CGC TTA CTG CCA GAA CAC AAA GCC AAG Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys 130 135 140	672
GCT CTG CTC TTT GAG GTA AAG GAG ATC TTC AGG AAG TCA CCT TTC CTG Ala Leu Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu 145 150 155	720
GTA CCA AAG GGC AGT GTT AGC ATC ATG GAT GGA TCC GAC GAA GGC ATA Val Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile 160 165 170	768
TTA GCT TGG GTT ACT GTG AAT TTT CTG ACA GGT CAG CTG CAT GGC CAC Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His 175 180 185 190	816
AGA CAG GAG ACT GTG GGG ACC TTG GAC CTA GGG GGA GCC TCC ACC CAA Arg Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln 195 200 205	864
ATC ACG TTC CTG CCC CAG TTT GAG AAA ACT CTG GAA CAA ACT CCT AGG Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg 210 215 220	912
GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT TAT AAG CTC TAT Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr 225 230 235	960

FIG. 7

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ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr 240 245 250	1008
CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser 255 260 265 270	1056
GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val 275 280 285	1104
AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCC Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro 290 295 300	1152
TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro 305 310 315	1200
GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp 320 325 330	1248
CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu 335 340 345 350	1296
AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu 355 360 365	1344
GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC ACC TAC Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr 370 375 380	1392
ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC Ile Thr Ala Leu Leu Lys Asp Gly Phe Ala Asp Ser Thr Val 385 390 395	1440
TTA CAG CTC ACA AAG AAA GTG AAC AAC ATA GAG ACG GGC TGG GCC TTG Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu 400 405 410	1488
GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT TGAGGCCAC Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His 415 420 425	1539
GTACTTCCTT GGAGACCTGC ATTTGCCAAC ACCTTTTAA GGGGAGGGAGA GAGCACTTAG TTCTGAACT AGTCTGGAC ATCCTGGACT TGAGCTAGA GATTTAGGTT TAATAATT TACACATCTA ATGTGAACTG CTGCCTAACCC ACTCAAGAGT ACACAGCTGG CACCAGAGCA TCACAGAGAG CCCTGTGAGC CAAAAAGTAT AGTTTTGGAA CTAAACCTTG GAGTGAGAGC CCAGGGACAG GTCCCTGGAA ACCAAAAGAAA AATCGCATTT CAACCCCTTG AGTGCCTCAT TCCACTGAAT ATTTAAATTT TCCTCTAAA TGGTAAACTG ACTTATATGCA ATCCCAAGAC CCATCAATAT CAGTATTTTT TTCCCTCCCTA TACAGTGCCC TGCCCCCCT TATCTGCACC CACCTCCCT GAAAAAGAGA GAAAAAAA AAAAAAAA	1599 1659 1719 1779 1839 1899 1959 1998

Fig. 7 (Cont'd.)

CD39L2	1	M K E G I R Y T E S R K T S Y I F Q Q P Q H G P W Q T R M R K I S H N H G S L R V A K V A Y P L G Q C V G V F	Y V A T H
CD39L4	1	-	-
CD39L1	1	-	-
CD39L3	1	-	-
CD39	1	-	-

ACR I

ACR II

CD39L2	120	PT-RPPFETPTLHEASCVVNPG-SAYAHVYKIAHQFPLVAVRQDIFDFWKEFPL
CD39L4	67	FVQKMPQQLPFLGEGVDSVPLPGCSAVLDFPLVQVPLGKLLLEVADIPRSKMRKPL
CD39L1	53	WPAKEKNDTGTIVCQHESVCDVPEFCISLWADHPSCLQHQLVGCQLEQALCDTPTPHEAATPL
CD39L3	75	WPAKEKNDTGTWOTKPSVVKGCSISYVWPTFVEREELCPLVAVGKPSCELGKPTPHEAATPL
CD39	67	WPAKEKNDTGTWHEVOMCIRVKGCGISKVVKVWVIVLTCERATVWVPSQHCPVTPHEAATPL

ACR II

CD39L2	178	VLKATAGCRLL...PCEKA....LKEKEPK...SPFLVGDDCVS...IDC...TCV...KLTIN
CD39L4	126	VLKATAGCRLL...PCEKA...LKEKEPK...SPFLVGDDCVS...IDC...TCV...KLTIN
CD39L1	118	MUGATAGCRLL...TNPETAT...TSV...LTHL...TQ...P...DFRGA...G...G...C...E...V...P...T...Y
CD39L3	135	MIGATAGCRLL...NET...A...T...V...L...S...O...Y...E...K...N...P...DFRGA...G...G...C...E...V...G...W...Y...T...Y
CD39	127	MIGATAGCRLL...NET...A...T...V...L...S...O...Y...E...K...N...P...DFRGA...G...G...C...E...V...G...W...Y...T...Y

ACR III

CD39L2	235	STGSSL...	ATPGGS...LVGLDLSG...STQI...FLPRV...ETLRA...SPH...GTYLTAGR...
CD39L4	183	STGSSL...	...GHC...P...G...L...L...G...G...G...T...F...L...P...G...L...L...D...O...P...G...Y...G...
CD39L1	176	AL...L...H...K...Y...G...N...Y...G...R...P...	...P...L...K...T...G...A...N...D...L...G...G...G...A...T...P...T...F...T...S...E...R...D...R...A...S...E...
CD39L3	193	ATGSG...R...G...H...L...H...H...M...M...	...P...H...G...C...D...T...T...S...S...L...D...L...G...G...G...C...T...I...P...A...G...K...D...L...G...G...S...D...E...N...G...O...S...L...

ACB IV

CD39L2	283	M-N-T-Y-K-L-Y-I-S-L-L-G-L-L-M-S-A-R-L-A-L-G-C-T-H-E-C-O-P-B-R-D-G-L-E-V-S-P-C-L-S-F-K-C-E-W-H-E-H-A-V-T-Y-R
CD39L4	231	H-E-S-T-Y-R-T-H-S-F-L-C-K-A-A-R-L-A-T-M-G-A-V-E-T-C-E-D-G-E-R-T-S-A-C-L-P-R-M-L-E-A-E-W-T-C-G-V-Y-A-W
CD39L1	229	Y-G-C-O-N-H-E-Y-T-H-S-F-L-C-Y-G-R-D-Q-V-L-O-R-E-L-A-S-A-J-O-...-T-C-H-E-P-C-L-P-R-G-F-S-I-V-L-E-G-U-D-Y-O-S
CD39L3	248	Y-G-C-Y-V-E-Y-T-H-S-F-L-C-O-Y-C-H-E-R-A-K-K-I-L-F-M-L-L-O-S-E-P-T-H-A-L-T-H-E-P-C-L-P-R-G-F-S-I-V-L-E-G-U-D-Y-O-S
CD39	242	Y-G-C-Y-V-E-Y-T-H-S-F-L-C-Y-C-H-E-R-A-K-K-I-L-F-M-L-L-O-S-E-P-T-H-A-L-T-H-E-P-C-L-P-R-G-F-S-I-V-L-E-G-U-D-Y-O-S

Fig. 8.

peaGDP	1	-----	-----	-----			
potapyrase	1	-----	-----	-----			
CD39L2	1	MKKGIRYETSRKTSYIFQQPQHGPWQTRM	K	HHGSLRVAEV	YPLGLCVGVF	Y	MHQH
CD39L4	1	-----	-----	-----	-----	-----	TSNG
dNTPase	1	-----	-----	-----	-----	-----	-----
yGDPase	1	-----	-----	-----	-----	-----	KPE
ACR I							
peaGDP	2	ELLIKLTPEFS	PLP	I	SSOYLGNN	..	-----
potapyrase	6	SEHFLPE	PLVPLPSL	S	EVVVAQI	P	-----
CD39L2	61	KMERATAQAFS	TR	PGARWGA	Q	..	-----
CD39L4	7	TEFF	LMVVCVCSAV	TR	PGFEGH	..	-----
dNTPase	37	KISFUCHIT	IL	PLVPGFV	SEKASP	..	-----
yGDPase	5	DISILP	ENDEPGY	QD	SKFVSKWV	Y	-----
ACR II							
peaGDP	61	EFNQNLDDLLHICKG	EVY	A	TPGLSSY	..	-----
potapyrase	63	PFHKLGLLPE	PL	SSY	PEOAKSLIPLL	Q	-----
CD39L2	119	QFT	PPRET	STL	THETPAV	KPLG	-----
CD39L4	66	TFVQ	PLVPLPSL	YADDV	EVK	IAFG	-----
dNTPase	96	KFNR	TFIDK	MLV	PLP	RELLDVA	QD
yGDPase	65	KF	TF	PL	PLP	SKFVSKWV	Y
ACR III							
peaGDP	121	REGATAGLRL	LN	GDA	AEKILQ	VRD	-----
potapyrase	123	ELC	ATAGLRL	LN	DAAEKILQ	AVR	-----
CD39L2	178	VLK	ATAGLRL	PLP	KA	K-L	OKP
CD39L4	126	VLK	ATAGLRL	PLP	KA	EV	PLP
dNTPase	156	VLK	ATAGLRL	PLP	SKA	EV	PLP
yGDPase	123	A	ATAGLRL	PLP	DAK	EV	PLP
ACR IV							
peaGDP	180	EGNLGR	TY	TVGV	DLGGGS	VA	-----
potapyrase	182	EGNLGR	TY	TVGV	DLGGGS	VA	-----
CD39L2	236	TGSLKTPGGS	..	AVG	LDLGGG	STCIA	-----
CD39L4	184	TGRLHCG	TY	TVGV	LDLGGG	STCIA	-----
dNTPase	214	EGRLSKTNQ	..	PLP	PLP	PEK	-----
yGDPase	183	EGNLGANG	PLP	TA	PLP	PEP	DPD
peaGDP	238	LYVH	SYLH	PLP	TA	PLP	PEP
potapyrase	239	LYVH	SYLH	PLP	TA	PLP	PEP
CD39L2	289	LYTH	SYLH	PLP	TA	PLP	PEP
CD39L4	237	LYTH	SYLH	PLP	TA	PLP	PEP
dNTPase	264	LYTH	SYLH	PLP	TA	PLP	PEP
yGDPase	238	LYQFS	SYLH	PLP	TA	PLP	PEP
peaGDP	276	LYSG	PLP	TA	PLP	PEP	PEP
potapyrase	277	LYGGV	PLP	TA	PLP	PEP	PEP
CD39L2	335	EN	EVTV	PLP	TA	PLP	PEP
CD39L4	282	GGV	Y	QGEV	PLP	PEP	PEP
dNTPase	308	LYGNV	Y	QGEV	PLP	PEP	PEP
yGDPase	298	LES	KTYT	PLP	PEP	PEP	PEP
peaGDP	332	PLASS	TY	PLP	PEP	PEP	PEP
potapyrase	333	PLASS	TY	PLP	PEP	PEP	PEP
CD39L2	379	PLA	FSY	TY	PLP	PEP	PEP
CD39L4	326	PLA	FSY	TY	PLP	PEP	PEP
dNTPase	360	PLA	FSY	TY	PLP	PEP	PEP
yGDPase	358	PLA	FSY	TY	PLP	PEP	PEP
peaGDP	392	PLCMD	LY	PLP	PEP	PEP	PEP
potapyrase	392	PLCMD	LY	PLP	PEP	PEP	PEP
CD39L2	428	PLCMD	LY	PLP	PEP	PEP	PEP
CD39L4	375	PLCMD	LY	PLP	PEP	PEP	PEP
dNTPase	406	PLCMD	LY	PLP	PEP	PEP	PEP
yGDPase	415	PLCMD	LY	PLP	PEP	PEP	PEP
peaGDP	452	MYFV
potapyrase	452	ASH*
CD39L2	483	ASH*
CD39L4	429	---
dNTPase	462	---
yGDPase	471	QSG

Fig. 9